```
10-615-383a-16. rag.
Title:
                    US- 10- 615- 383A- 16
Perfect score:
                    51
                    1 TYTFTDYVD 9
Sequence:
PN
      WO9748727- A1.
XX
PD
      24- DEC- 1997.
XX
PF
      18-JUN-1997;
                         97WO-SE001091.
XX
PR
XX
      20-JUN-1996:
                         96SE-00002496.
PΑ
      (GUSS/)
                GUSS B
PA
PA
PA
                NI LSSON M
       NI LS/ )
      (FRYK/)
                FRYKBERG L.
      (FLCC/) FLCCK J.
PA
      (LIND/) LINDBERG M
XX
PI
XX
      Guss B,
                Nilsson M,
                                 Frykberg L, Flock J, Lindberg M,
DR
      WPI; 1998-063079/06.
      N- PSDB; AAV04279.
PC: NCBI; gi 3201550.
DR
Fibri nogen-binding protein from coagul ase-negative Staphyl ococcus - used
      for prevention, treatment and diagnosis of Staphylococcus infection.
      Example 3; Fig 6; 45pp; English.
      The protein comprises the fibrinogen binding protein (FIG) of coagulase-
      negative Staphylococcus epiderm dis HB. Its am no acid sequence was
      deduced from the isolated fig gene (see AAV04279). The closest known
      analogue of FIG is the clumping factor of S. aureus which also binds
      fibrinogen and promotes bacterial aggregation in serum Recombinant FIG polypeptides can be expressed in host cells. They are used as immunogens,
      particularly in vaccines (which may be expressed in vivo) to protect
      humans and animals against coagulase-negative Staphylococcus infection. Antibodies raised against FIG can be used for passive immunisation. They block the adherence of bacteria) and for diagnosis. (Updated on 17-CCT-
      2003 to standardise OS field)
      Revised record issued on 18-OCT-2007: Enhanced with precomputed
      information from BOND.
X
SQ
      Sequence 1092 AA;
  Query Match 100.0% Score 51; DB
Best Local Similarity 100.0% Pred. No. 25;
Matches 9; Conservative 0; M smatches
                                                         DB 2; Length 1092;
                9; Conservative
                                                                0; Indels
                                                                                  0:
                                                                                       Gaps
                                                                                                 0:
Qy
               1 TYTFTDYVD 9
            372 TYTFTDYVD 380
Db
US- 10- 615- 383A- 10
Perfect score:
                    4824
                    1 LKKNNLLTKKKPI ANKSNKY......FAGLGALLLGKRRKNRKNKN 930
Sequence:
```

- 10- 615- 383a- 10. r ag.

```
WO9748727- A1.
XX
PD
XX
PF
XX
PR
XX
      24- DEC- 1997.
                        97WO-SE001091.
      18-JUN-1997;
      20-JUN-1996;
                        96SE-00002496.
PA
      (GUSS/)
                GUSS B.
PΑ
                NI LSSON M
       NI LS/)
PA
      (FRYK/)
                FRYKBERG L.
PA
      FLOC/ )
                FLOCK J.
      LIND/
PA
               LI NDBERG M
XX
PΙ
                 Nilsson M,
                                Frykberg L, Flock J, Lindberg M,
      Guss B,
XX
DR
      WPI: 1998-063079/06.
      N- PSDB; AAV04279.
PC: NCBI; gi 3201550.
DR
DR
Fibrinogen-binding protein from coagulase-negative Staphylococcus - used
      for prevention, treatment and diagnosis of Staphylococcus infection.
      Example 3; Fig 6; 45pp; English.
      The protein comprises the fibrinogen binding protein (FIG) of coagulase-
      negative Staphylococcus epiderm dis HB. Its am no acid sequence was deduced from the isolated fig gene (see AAV04279). The closest known analogue of FIG is the clumping factor of S. aureus which also binds
      fibrinogen and promotes bacterial aggregation in serum Recombinant FIG polypeptides can be expressed in host cells. They are used as immunogens, particularly in vaccines (which may be expressed in vivo) to protect humans and animals against coagulase-negative Staphylococcus infection.
      Antibodies raised against FIG can be used for passive immunisation. They
      block the adherence of bacteria) and for diagnosis. (Updated on 17-OCT-
      2003 to standardise OS field)
      Revised record issued on 18-OCT-2007: Enhanced with precomputed
      information from BOND.
      Sequence 1092 AA;
  Query Match
                                93.0%
                                          Score 4485;
                                                          DB 2;
                                                                   Length 1092;
  Best Local Similarity
                                81.1%
                                          Pred. No. 2.4e-212;
                                       19:
                                                              27:
  Mat ches
             883:
                   Conservative
                                              M smat ches
                                                                    Indels 160;
                                                                                     Gaps
                                                                                               3:
               2 KKNNLLTKKKPI ANKSNKYAI RKFTVGTASI VI GAALLFGLGHNEAKAEENTVQDVKDSN 61
Qy
                 KKNNLLTKKKPI ANKSNKYAI RKFTVGTASI VI GATLLFGLGHNEAKAEENSVQDVKDSN 63
Db
Qy
             62 MDDELSDSNDQSSNEEKNDVINNSQSINTDDDNQ-IKKEETNSNDAIENRSKDITQSTTN 120
                 Db
            121 VDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTI NSEASI QTSDNE 180
Qy
Db
            181 ENSRVSDFANSKI I ESNTESNKEENTI EQPNKVREDSI TSQPSSYKNI DEKI SNQDELLN 240
Qy
                 EDSHVSDFANSKI KESNTESÇKEENTI EÇPNKVKEDSTTSÇPSĞYTNI DEKI SNÇDELLN
Db
            241 LPI NEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLI KVTDQSI TEGYDDSDGI I 300
Qy
                                                Page 2
```

Untitled

Db	244	LPI NEYENKARPLSTTSAQPSI KRVTVNQLAAEQQSNVNHLI KVTDQSI TEGYDDSEGVI	303
Qy	301	KAHDAENLI YDVTFEVDDKVKS@DTMTVNI DKNTVPSDLTDSFAI PKI KDNSŒI I ATGT	360
Db	304		363
Qy	361	YDNTNKQI TYTFTDYVDKYENI KAHLKLTSYI DKSKVPNNNTKLDVEYKTALSSVNKTI T	420
Db	364	YDNKNKO TYTETDYVDKYENI KAHLKLTSYI DKSKVPNNNTKLDVEYKTALSSVNKTI T	423
Qy	421	VEYQKPNENRTANLQSMFTNI DTKNHTVEQTI YI NPLRYSAKETNVNI SQNGDEGSTI I D	480
Db	424	VEYGRPNENRTANLOSMFTNI DTKNHTVEQTI YI NPLRYSAKETNVNI SONODEOSTI I D	483
Qy	481	DSTI I KVYKVQDNQNL PDSNRI YDYSEYEDVTNDDYAQLGNNNDVNI NFGNI DSPYI I KV	540
Db	484	bsti i kvykvabnanlebsniki ybyseyebvtnibbyaalanninbvni neani bseyi i kv	543
Qy	541	I SKYDPNKDDYTTI QQTVTMQTTI NEYTŒFRTASYDNTI AFSTSSGQGQGDLPPEKTYK	600
Db	544	Í SKÝDPNKODÝTTÍ COTVTMOTTÍ NEÝTŒFRTÁSÝDNTÍ ÁFSTSSECCICICIÓL PPEKTÝK	603
Qy	601	I GDYVWEDVDKDGI QNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEEGKYQFDGLKNGLTY	660
Db	604	I GDYVWEDVDKDGI GNTNDNEKPLSNVLVTLTYPDGTSKSVRTDEDGKYQFDGLKNGLTY	663
Qy	661		
Db	664	KI TFETPEGYTPTLKHSGTNPALDSEGNSVWYTI NGQDDMTI DSGFYQTPKYSLGNYVWY	723
Qy	721		
Db	724	DTNKDGI QQDDEKGI SĞVKVTLKDENGNI I STTTTDENGKYQFDNLNSGNYI VHFDKPSG	783
Qy	781		833
Db	784	MTQTTTDSQDDDEQDADQEEVHVTI TDHDDFSI DNGYYDDESDSDSDSDSDSDSDSDSDSDSDSDSDS	843
Qy	834		833
Db	844		903
Qy	834		833
Db		DS	
Qy	834	DSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDS	
Db	964	DS	
Qy	881		
Db		GSDSDSDSDSDSDNDSDLGNSSDKSTKDKLPDTGANEDYGSKGTLLGTLFAGLGALLLGK	1083
Qy		RRKNRKNKN 930	
Db	1084	RRKNRKNKN 1092	